IRSTI 68.39.15 https://doi.org/10.52081/bkaku.2026.v76.i1.319

ASSESSMENT AND PREDICTION OF THE BREEDING VALUE OF HOLSTEIN BULLS USING GENOMIC ANALYSIS

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Annotation. The article presents the results of establishing a Kazakhstan reference population of the Holstein breed and assessing the breeding value of animals based on genomic analysis. A reliable database was developed for first-lactation cows based on 305-day lactation records, including the collection and genotyping of 2,980 biological samples using a panel of more than 50,000 SNP markers. Biological material was obtained from animals in nine breeding farms involving 89 service sires, ensuring sample representativeness and broad genetic coverage. Based on calculated genomic estimated breeding values (GEBV), a comprehensive Genomic Holstein Global Index (GHGI) was developed, incorporating milk production traits, conformation, health, longevity, and manageability. The distribution of GHGI and GEBV for milk yield approximated normality with slight positive skewness, indicating targeted selection of animals with high genetic potential. Carriers of hereditary anomalies HH1, HH3, HH4, HH5, and CVM were identified at low frequencies, emphasizing the necessity of genetic monitoring in breeding programs. The results confirm the effectiveness of integrated genomic selection for accelerating genetic progress, improving productivity, and ensuring genetic safety of the Holstein population under Kazakhstan conditions.

Keywords: genomic selection, Holstein breed, breeding value, GEBV, SNP markers, reference population, GHGI.

Introduction. The development of dairy cattle breeding requires the implementation of scientifically grounded methods for evaluating and selecting breeding stock, which is particularly important for high-producing breeds such as Holstein. This breed occupies a leading position in the global dairy industry due to its high milk yield, milk quality, and adaptability to diverse climatic conditions. Sustainable productivity improvement requires not only phenotypic selection but also the integration of animals' genetic potential into breeding programs. Effective selection of service sires capable of transmitting desirable traits – milk yield, milk composition, health status, and reproductive performance – requires predictive models for breeding value estimation. Traditionally, breeding value estimation relied on phenotypic data and milk composition, incorporating information on the individual, its ancestors, and progeny [1]. However, such approaches are time-consuming, costly, and susceptible to environmental effects.

Genomic technologies provide new opportunities. SNP marker analysis and calculation of genomic estimated breeding values (GEBV) enable early selection, reduction of the generation interval, and acceleration of genetic progress [2]. A key component of genomic evaluation is the establishment of a reference population comprising animals with highly reliable progeny-based evaluations and genomic information, as the accuracy of GEBV strongly depends on the quality of this reference base [3].

Milk production performance in dairy cows is commonly evaluated on the basis of the standardized 305-day lactation period (test-day milk yield, fat content, and protein content). However, averaging environmental effects across the entire lactation cycle may lead to underestimation of daily variability in influencing factors and, consequently, to distortion of genetic and paratypic parameters as well as estimated breeding values [4]. Therefore, current trends increasingly support the implementation of dynamic models that account for variability in environmental factors at different stages of lactation.

Furthermore, investigation of the genetic architecture of productive and adaptive traits demonstrates that most of these traits are polygenic in nature, meaning that numerous genes with small effects contribute to trait expression. In this context, marker-assisted selection (MAS), based on individual genes or quantitative trait loci (QTL), proves to be limited in scope [5]. Contemporary genome-wide association studies (GWAS) identify numerous genomic regions associated with economically important traits, which necessitates the application of statistical methods capable of handling a large number of markers with a comparatively smaller number of individuals, including BLUP, RR-BLUP, Bayes-R, PLSR, SVR, and others [6]. The selection of the most appropriate method for calculating genomic estimated breeding values is a key determinant of prediction accuracy and the overall efficiency of the breeding program [7].

In the context of Russia and Kazakhstan, the integration of modern breeding and technological approaches is of particular importance. In Kazakhstan, despite the presence of local breeds and imported genetic lines, herd productivity remains below the potential achievable by the Holstein breed in favorable production environments, which necessitates intensified genetic improvement and the implementation of genomic technologies [8]. At the same time, preservation of genetic diversity, minimization of inbreeding, and adaptation of breeds to regional climatic conditions represent critical priorities.

Scientifically substantiated breeding and technological programs provide the foundation for the targeted improvement of breed composition, ensuring a comprehensive approach to animal selection based on productive and adaptive traits. Within such programs, optimization of breeding structure and application of genetic and statistical analytical methods enhance the efficiency of the selection process. The implementation of these approaches contributes to the preservation of unique biological characteristics of local breeds, their adaptation to modern production systems, increased productivity, and strengthening of overall disease resistance.

The implementation of such programs is essential for maintaining biological diversity and ensuring food security, as animal resilience to diseases, climatic stressors, and environmental changes constitutes a key factor in the stable development and ecological sustainability of livestock production.

Modern dairy cattle breeding is undergoing a phase of profound technological modernization that requires the integration of classical phenotypic methods with advanced genomic, analytical, and digital tools. The comprehensive application of these approaches ensures not only more accurate estimation of breeding value and genetic potential, but also facilitates the development of long-term breeding strategies aimed at improving productivity, reproductive performance, and disease resistance [9].

The application of genomic technologies in combination with digital herd management systems enables the creation of intelligent databases, real-time monitoring of production indicators, and prediction of heritable traits based on large-scale datasets. This contributes to accelerated genetic progress, reduction of inbreeding, and preservation of genetic diversity [10,11].

Thus, effective development of the industry is impossible without the implementation of integrated selection methods that combine traditional and innovative approaches. Their rational integration ensures the formation of highly productive, stress-resistant, and economically efficient herds, which constitutes a key condition for the sustainable development of dairy cattle breeding under conditions of global climate change and increasing product quality requirements [12-15].

Objectives:

– To establish a reliable pedigree and performance database for first-lactation Holstein cows based on 305-day lactation records, including the collection of biological samples and expansion of the DNA gene bank to no fewer than 2,500 samples. Genotyping of no fewer than 2,500 biological samples from first-lactation Holstein black-and-white cows will be performed using a panel of at least 50,000 SNP markers.

– To collect data from Holstein service sires.

– To conduct a bioinformatic analysis of the relationship between genes and phenotypic traits in no fewer than 2,500 first-lactation Holstein black-and-white cows.

Materials and Methods. Biological material, represented by tail hair samples with follicles, was collected to establish a DNA database for no fewer than 2,500 Holstein cows included in the Kazakhstan reference population. The collected samples were placed in specialized hair-collection envelopes manufactured in accordance with Patent of the Republic of Kazakhstan for a utility model No. 5749 dated 08.01.2021, entitled "Envelope for Hair Collection, Method of Its Manufacture and Use." Genotyping of more than 2,500 biological samples obtained from first-lactation Holstein black-and-white cows, including no fewer than 50,000 SNP markers, was carried out in an accredited laboratory operating in accordance with international standards and the recommendations of ICAR (Hungarian Holstein-Friesian Breeders Association).

Biological material was collected from breeding animals participating in the selection and breeding program and registered in the Republican Chamber of Dairy and Dual-Purpose Cattle Breeds. Sampling was conducted exclusively from animals for which the following information was available:

– individual identification number (KZ);

– inventory or farm number (and, where available, tattoo), and registration number in the breed registry;

– information on date of birth, breed, and owner of the animal.

For DNA extraction, clean hair samples with intact follicles were used in a quantity of no fewer than 50 hairs per animal. Sampling was performed by program executors in cooperation with farm specialists in strict compliance with animal identification requirements and packaging regulations using specialized envelopes. Data on cow productivity (milk yield, fat and protein content in milk, somatic cell count), as well as information on Holstein service sires, were obtained through data extraction from the Republican Livestock System database "Information and Analytical System."

Within this framework and in accordance with the approved work plan, extensive work was carried out to establish a reliable database of breeding animals of the Holstein black-and-white breed. The database includes information on first-lactation cows for the 305-day lactation period, their pedigree, productive performance indicators, and physiological status. Simultaneously, biological samples were collected for subsequent genetic analysis, which substantially expanded the existing DNA gene bank, with the total number of samples exceeding 2,500 units.

The collected information was systematized and analyzed to ensure completeness and representativeness of the data required for genomic research. During the reporting year, work on expanding the Holstein reference population database was continued: in addition to the biological samples collected in 2024 (1,011 head), 2,980 new samples obtained from nine core farms were included.

In addition, data on Holstein service sires were collected and structured, including information on pedigree, qualitative and quantitative semen characteristics, and results of progeny performance. The obtained data formed the basis for further bioinformatic analysis of associations between genetic markers and phenotypic traits and ensured a high level of reliability and representativeness of the studied sample across the entire population (Table 1).

Analysis of the data presented in Table 1 demonstrates that 2,980 biological samples obtained from animals belonging to nine core farms were included in the study, involving 89 service sires. The largest number of samples was obtained from LLP "Bek+" (590 units), LLP

"OHMK" (508 units), and LLP "AF Rodina" (492 units), indicating a substantial herd size and a systematic approach to breeding record management in these enterprises. A considerable number of samples (445 units) was also provided by LLP "RULIKHA," where a significant number of service sires (22 head) are utilized, ensuring broad genetic diversity.

Table 1 – Collection of biological samples

No.	Farm	Number of Samples	Service Sires
1	LLP "Sharkul Food"	123	8
2	LLP "ZKAP Amiran"	100	13
3	LLP "AIS"	284	10
4	Peasant Farm "Aidarbayev Erik Serikovich"	100	11
5	LLP "Bek+"	590	22
6	LLP "AF Rodina"	492	26
7	LLP "OHMK"	508	10
8	LLP "RULIKHA"	445	22
9	LLP "AgroTradeRV"	338	16
	TOTAL:	2980	89

Analysis of the data presented in Table 1 demonstrates that 2,980 biological samples obtained from animals belonging to nine core farms were included in the study, involving 89 service sires. The largest number of samples was obtained from LLP "Bek+" (590 units), LLP "OHMK" (508 units), and LLP "AF Rodina" (492 units), indicating a substantial herd size and a systematic approach to breeding record management in these enterprises. A considerable number of samples (445 units) was also provided by LLP "RULIKHA," where a significant number of service sires (22 head) are utilized, ensuring broad genetic diversity.

Farms with smaller sample sizes (LLP "Sharkul Food," LLP "ZKAP Amiran," and Peasant Farm "Aidarbayev E.S.") make an important contribution to the development of a representative database by ensuring coverage of diverse regional management and feeding conditions.

Analysis of the origin of service sires revealed that semen from imported animals originating from leading breeding centers in the United States, Canada, Germany, and Denmark was predominantly used in reproduction programs. The average milk yield of daughters of sires from the United States was 12,210 kg, from Canada – 11,947 kg, from Germany – 11,350 kg, and from Denmark – 11,090 kg, indicating the high genetic merit of the germplasm utilized.

Thus, the structure of the collected biological samples and the broad genetic representation of service sires provide a solid foundation for reliable genomic research aimed at estimating breeding value and improving the productive traits of Holstein cattle under the conditions of Kazakhstan.

The collection of biological samples was carried out in accordance with established requirements using specialized hair-collection envelopes (Patent of the Republic of Kazakhstan No. 5749), ensuring preservation of the material and its suitability for subsequent genetic analysis. Information on animal pedigree was obtained from official internal breeding information systems and from the Information and Analytical System of the Republican Livestock System (IAS "RLS") (https://plem.kz), which guarantees the reliability of pedigree data.

As a result of the work performed, the biological sample database was supplemented with materials from 2,980 head of cattle. For each sample, in accordance with the requirements of the foreign genetic laboratory, identification data were recorded, including the individual animal identification number, date of birth, identification number of the sire, and identification number of the maternal grandsire. This level of detail ensures accurate tracing of genealogical relationships and proper genotyping in accordance with international standards of genomic research.

The collected 2,980 biological samples, together with complete animal information, were transferred to the foreign laboratory of the Hungarian Holstein Association for genetic analysis. The transfer of material was accompanied by full documentation of identification data, ensuring the accuracy of genotyping procedures and enabling subsequent analysis of associations between genetic markers and phenotypic traits. The obtained results will be used for estimating the breeding value of animals and for improving breeding programs in Kazakhstan.

Genetic evaluation of genomic estimated breeding values (GEBV) was performed for the genotyped DNA biological samples, on the basis of which the Genomic Holstein Global Index (GHGI, Figure 1) was calculated. The index includes a composite set of indicators: milk production (45%, of which 15% corresponds to fat yield and 30% to protein yield), conformation (32%, including 16% for the udder index and 16% for the feet and legs index), health (10%, based on somatic cell count), productive longevity (10%), and manageability (3%, reflecting calving ease). In addition, detailed evaluations of individual components are presented, including milk production, conformation traits, udder health status, as well as identified genetic anomalies and deviations typical for the Holstein breed.

The distribution of GHGI values within the studied animal population, presented in Figure 1, approximates normality and is characterized by a moderate concentration of values around the mean. This indicates the absence of pronounced asymmetry and suggests that the majority of animals possess genetic potential close to the average GHGI level. At the same time, individual animals demonstrate higher or lower values, reflecting genetic variability within the population and allowing its consideration in breeding planning.

Analysis of the GHGI (Genomic Holstein Genetic Index) distribution makes it possible to identify the most promising animals for targeted selection in breeding programs, serving as a key instrument for enhancing the efficiency of genetic progress. Particular attention is recommended for individuals with high scores in milk production, conformation, and functional traits, as these animals are capable of ensuring accelerated improvement of productive and reproductive characteristics of the entire herd.

Furthermore, control of udder health, reproductive performance, and manageability constitutes an integral component of the breeding program, enabling minimization of risks associated with mastitis, metabolic disorders, and management difficulties, as well as reduction of economic losses at the farm level. Systematic monitoring of GHGI in combination with clinical observation and accurate pedigree documentation makes it possible not only to select genetically superior animals, but also to maintain herd health stability and adaptive capacity.

Thus, the application of GHGI in breeding practice ensures a comprehensive approach to evaluating the genetic merit of animals, promotes conservation and rational utilization of genetic diversity, and optimizes the genomic selection program for the Holstein breed. This enables the formation of a highly productive, stress-resistant, and economically efficient herd, which represents a strategically important objective for modern dairy cattle breeding.

The distribution of the Genomic Holstein Global Index (GHGI, Figure 1) demonstrates a slight rightward shift, indicating a predominance of genotyped animals with index values above the population mean. This pattern reflects the targeted selection of high-potential animals for genotyping, including heifers and young bulls from which optimal milk production, conformation, and health performance are expected. The focus on genetically superior individuals indicates the strategic use of genomic information by herd managers for mating planning, herd replacement decisions, and selection of young sires. This approach creates conditions for accelerated genetic progress and improvement of productive and functional characteristics of the national Holstein population.

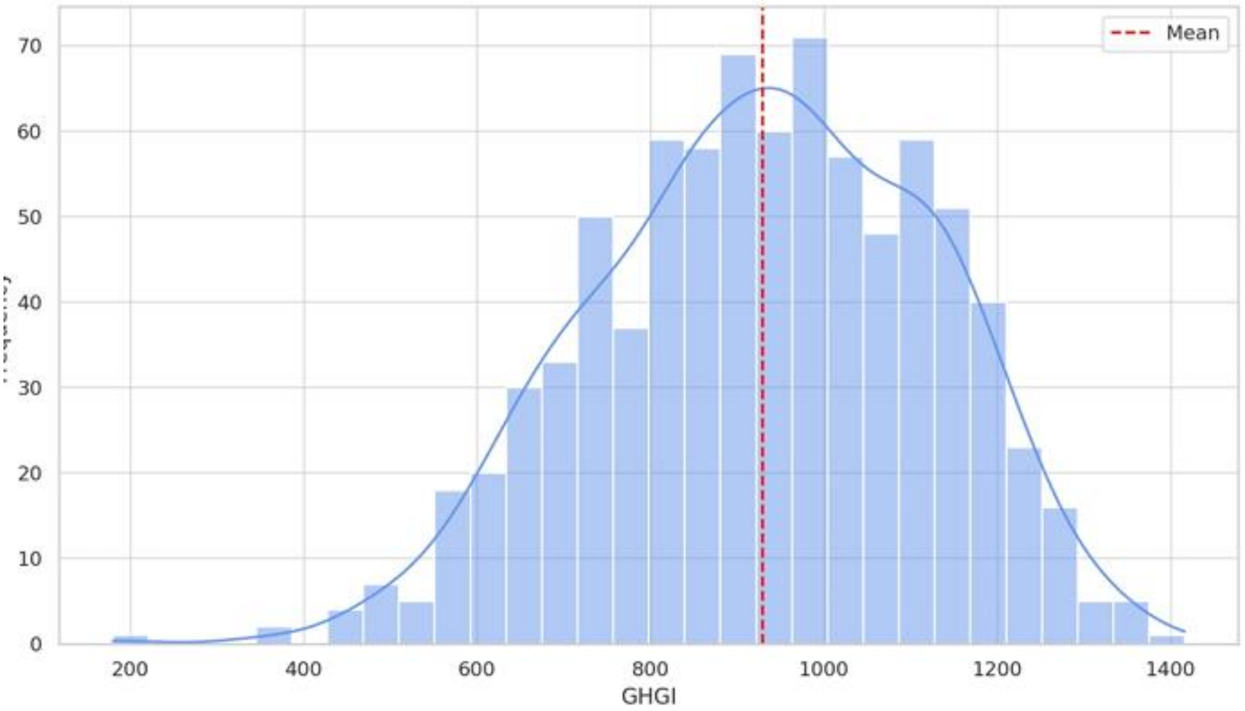

Figure 1 – Distribution of GHGI Scores

Analysis of the obtained genomic estimated breeding values (GEBV) indicates that GHGI integrates a comprehensive set of traits: milk production (45%, including 15% fat yield and 30% protein yield), conformation (32%, of which 16% corresponds to the udder index and 16% to the feet and legs index), health (10%, based on somatic cell count), productive longevity (10%), and manageability (3%, reflecting calving ease). Such a multifactorial evaluation allows simultaneous consideration of productive, functional, and biological characteristics of animals, which is essential for population-level breeding programs.

Genetic analysis of the reference population revealed the presence of carriers of several genetic disorders and anomalies that may lead to economic losses and reduced reproductive efficiency. Of the 18 investigated pathologies, 6 were not detected in the population, indicating positive outcomes of previous selection measures and a reduction in the frequency of hereditary defects. At the same time, the following genetic anomalies were identified:

– HH1 (Holstein Haplotype 1) – a lethal or sublethal mutation causing embryonic mortality in the homozygous state; detected in 0.46% of the population;

– HH3 (Holstein Haplotype 3) – a mutation in the SMC2 gene leading to arrest of early embryonic development (30–60 days of gestation); identified in 1.68% of animals;

– HH4 (Holstein Haplotype 4) – a mutation in the TRAF6 gene affecting immune response and resulting in late embryonic mortality in homozygotes; recorded in 0.76%;

– HH5 (Holstein Haplotype 5) – a lethal recessive mutation causing embryonic death between 35 and 90 days of gestation; observed in 1.37%;

– CVM (Complex Vertebral Malformation) – a congenital vertebral defect leading to abortion or the birth of non-viable calves; detected in 0.15% of the population.

Analysis of carrier frequency underscores the necessity of a systematic approach to selection and genetic safety control in herds. Regular screening of young stock for the detection of carriers of deleterious alleles is particularly important, as it enables their exclusion from breeding programs, reduces the risk of economic losses, and enhances population sustainability.

The data further demonstrate that the strategic selection of high-potential animals for genotyping and breeding contributes to the concentration of favorable genetic factors within the population. In the long term, this creates a foundation for sustainable improvement of milk productivity, enhancement of conformation and udder health, reduction of somatic cell counts, and mitigation of reproductive risks.

Thus, the results of the GHGI analysis and the identification of genetic anomalies confirm the effectiveness of integrated genomic selection and highlight the necessity of continued monitoring and further development of the Holstein reference population with consideration of hereditary diseases. Implementation of recommendations aimed at excluding carriers of undesirable alleles ensures long-term genetic progress, increased productivity, and improved economic efficiency in dairy cattle breeding.

The analysis of GEBV estimates for productive traits, particularly milk yield, demonstrated an appropriate distribution of values within the population, as illustrated in Figure 2, indicating a balanced genetic potential of the herd.

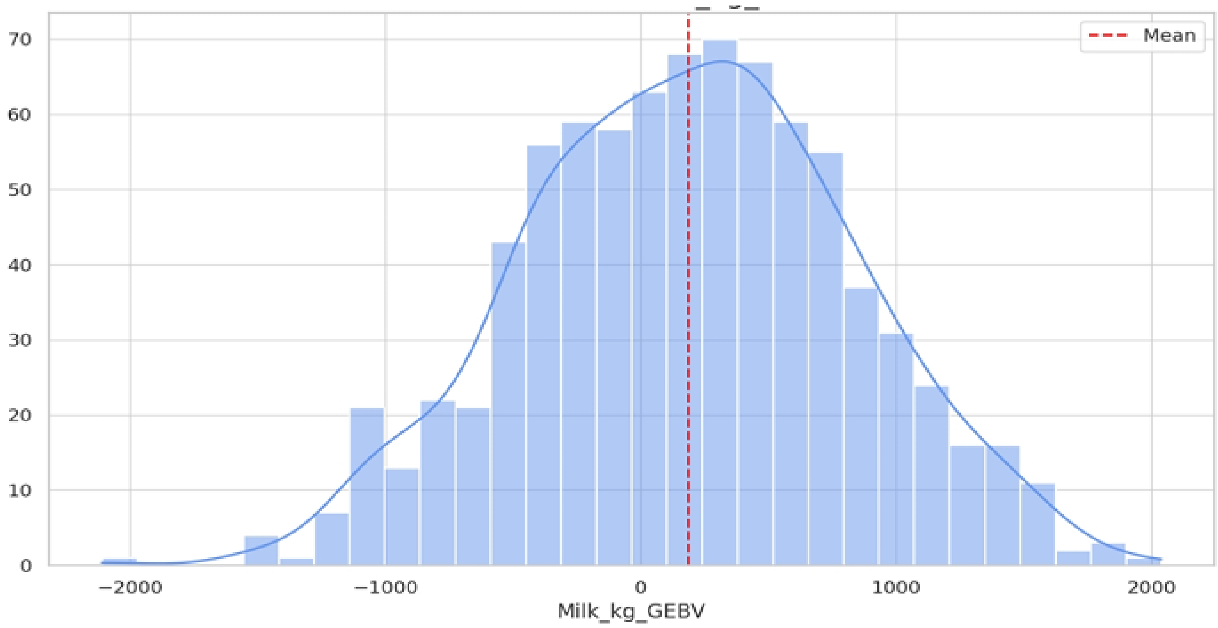

Figure 2 – Distribution of GEBV estimates for milk yield, kg

As shown in Figure 2, the distribution of estimated breeding values for milk yield in the studied population approximates normality, with a uniform dispersion around the mean. A slight shift of the distribution toward higher values indicates that breeders select animals for genotyping from families with confirmed above-average productivity. This strategy is aimed at the early identification of the most promising individuals possessing high genetic potential, thereby enabling prediction and enhancement of herd productivity throughout the productive lifetime of cows.

Within the framework of developing the reference population, work is ongoing on the development and implementation of a technology for predicting the breeding value of Holstein service sires based on genomic analysis. This approach ensures the integration of data on milk production, conformation, health, and reproductive traits, enabling scientifically substantiated breeding decisions and contributing to accelerated genetic progress within the national population.

Conclusion. The database of Holstein breeding animals was expanded by 2,980 biological samples obtained from nine core farms with the participation of 89 service sires. The largest number of samples was received from LLP “Bek+” (590 units), LLP “OHMK” (508 units), and LLP “AF Rodina” (492 units), ensuring broad genetic coverage and representativeness of the sample. All biological samples were accompanied by detailed identification information and transferred to a foreign laboratory for genetic analysis, thereby establishing a reliable foundation for breeding value estimation and improvement of Holstein cattle productivity in Kazakhstan.

Calculation of the Genomic Holstein Global Index (GHGI) based on genomic estimated breeding values for 2,980 samples incorporated milk production (45%), conformation (32%), health (10%), productive longevity (10%), and manageability (3%). The distribution of GHGI approximated normality with a slight rightward shift, reflecting the concentration of high-potential animals. Carriers of genetic anomalies HH1, HH3, HH4, HH5, and CVM (0.15–1.68%) were identified, necessitating control within breeding programs. Evaluation of GEBV for milk yield demonstrated a normal distribution with a slight shift toward higher values, confirming the appropriateness of the selection strategy. The application of GHGI together with data on hereditary defects enables the selection of animals with high productivity and superior conformation while minimizing reproductive and genetic risks. The implementation of this integrated approach ensures accelerated genetic progress and increased economic efficiency of dairy herds.

Financing. This research was funded by the Ministry of Agriculture of the Republic of Kazakhstan (program No. BR22886157 «Management, conservation and rational use of genetic resources of cattle of dairy breeds with by means of selection and technological and molecular genetic methods») 2024-2026y.

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ГОЛШТИН ТҰҚЫМДЫ БҰҚАЛАРДЫҢ ГЕНОМДЫ БАҒАЛАУ НЕГІЗІНДЕГІ АСЫЛ ТҰҚЫМДЫҚ ҚҰНДЫЛЫҒЫН АНЫҚТАЙ ОТЫРЫП БОЛЖАМ ЖАСАУ

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Аңдатпа. Мақалада Қазақстан жағдайында голштин тұқымы бойынша референттік популяцияны қалыптастыру және жануарлардың асыл тұқымдық құндылығын геномдық талдау негізінде бағалау нәтижелері ұсынылған. 305 күндік лактациядағы бірінші бұзаулаған сиырлардың деректері бойынша сенімді мәліметтер базасы құрылып, 50 мыңнан астам SNP-маркерлер панелі арқылы 2980 биологиялық үлгі іріктеліп, генотиптелді. Биоматериал тоғыз асыл тұқымды шаруашылықтағы 89 аталық бұқаның ұрпақтарынан алынып, зерттеу таңдауының репрезентативтілігін және генетикалық қамтылу ауқымының кеңдігін қамтамасыз етті. Есептелген геномдық асыл тұқымдық құндылықтар (GEBV) негізінде сүт өнімділігі, экстерьер, денсаулық, шаруашылықта пайдалану ұзақтығы және басқарылу көрсеткіштерін біріктіретін голштин тұқымының кешенді геномдық жаһандық индексі (GHGI) анықталды. GHGI мен сүт өнімі бойынша GEBV көрсеткіштерінің таралуы қалыпты үлестірімге жақын болып, жоғары мәндер жағына аздаған ығысу байқалды, бұл жоғары генетикалық әлеуеті бар жануарларды мақсатты іріктеуді көрсетеді. HH1, HH3, HH4, HH5 және CVM тұқым қуалайтын аномалияларының тасымалдаушылары төмен жиілікпен анықталды, бұл асылдандыру жұмыстарында генетикалық мониторинг жүргізудің маңыздылығын дәлелдейді. Алынған нәтижелер Қазақстан жағдайында голштин тұқымы популяциясының генетикалық қауіпсіздігін қамтамасыз ету, өнімділігін арттыру және генетикалық прогресті жеделдету үшін интеграцияланған геномдық селекцияның тиімділігін растайды.

Тірек сөздер: голштин тұқымы, геномдық селекция, асыл тұқымдық құндылық, GEBV, GHGI, SNP-маркерлер, референттік популяция.

ПРОГНОЗИРОВАНИЕ ПЛЕМЕННОЙ ЦЕННОСТИ БЫКОВ ГОЛШТИНСКОЙ ПОРОДЫ НА ОСНОВЕ ГЕНОМНОЙ ОЦЕНКИ

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Аннотация. В статье представлены результаты формирования казахстанской референтной популяции по голштинской породе и оценки племенной ценности животных на основе геномного анализа. На основе данных по коровам-первотёлкам за 305-дневную лактацию была сформирована достоверная база данных, отобрано и генотипировано 2980 биологических образцов с использованием панели более чем из 50 тыс. SNP-маркеров. Биоматериал был получен от потомков 89 быков-производителей из девяти племенных хозяйств, что обеспечило репрезентативность выборки и широкий охват генетического разнообразия популяции.

На основе рассчитанных геномных племенных ценностей (GEBV) определён комплексный геномный глобальный индекс голштинской породы (GHGI), объединяющий показатели молочной продуктивности, экстерьера, здоровья, продолжительности хозяйственного использования и управляемости стада. Распределение показателей GHGI и GEBV по молочной продуктивности было близким к нормальному, с незначительным смещением в сторону более высоких значений, что свидетельствует о целенаправленном отборе животных с высоким генетическим потенциалом.

Носители наследственных аномалий HH1, HH3, HH4, HH5 и CVM выявлены с низкой частотой, что подтверждает важность проведения генетического мониторинга в племенной работе. Полученные результаты подтверждают эффективность интегрированной геномной селекции для обеспечения генетической безопасности популяции голштинской породы в условиях Казахстана, повышения её продуктивности и ускорения генетического прогресса.

Ключевые слова: голштинская порода, геномная селекция, племенная ценность, GEBV, GHGI, SNP-маркеры, референтная популяция.